

ABSTRACT OF THE DISCLOSURE

A method that enables defining relationships between data points (e.g. genes).

The method disclosed is not limited by the size of the data set, the potentially misleading effect of background noise is reduced, relationship are not distorted, and that allows for comprehensible graphical presentation. The disclosed method solves the problem of visualization, analysis and interpretation of complex, multi-dimensional data. Such data may consist of data points from expression profiling analysis, 2D gel electrophoresis or SNP analysis. Here, multiple data sets exist and only the integration of all the sets into a two dimensional representation permits an analysis that allows the extraction of the information with respect to what events best explain the status of the cell, for example.